We claim:

1. A method for the fermentative production of at least one sulfur-containing fine chemical, which comprises the following steps:
   a) fermentation of a coryneform bacteria culture producing the desired sulfur-containing fine chemical, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity;
   b) concentration of the sulfur-containing fine chemical in the medium or in the bacterial cells, and
   c) isolation of the sulfur-containing fine chemical.

2. A method as claimed in claim 1, wherein the sulfur-containing fine chemical comprises L-methionine.

3. A method as claimed in either of the preceding claims, wherein the heterologous metA-encoding nucleotide sequence is less than 100% homologous to the metA-encoding sequence from Corynebacterium glutamicum ATCC 13032.

4. A method as claimed in claim 3, wherein the metA-encoding sequence is derived from any of the following organisms:

Corynebacterium diphteriae	ATCC 14779
Mycobacterium leprae	ATCC 43910
Mycobacterium tuberculosis CDC1551	ATCC 25584
Chlorobium tepidum	ATCC 49652
Pseudomonas aeruginosa	ATCC 17933
Caulobacter crescentus	ATCC 19089
Neisseria gonorrhoeae	ATCC 53420
Neisseria meningitidis	ATCC 53414
Pseudomonas fluorescens	ATCC 13525
Burkholderia cepacia	ATCC 25416
Nitrosomonas europaea	ATCC 19718
Haemophilus influenzae	ATCC 51907
Halobacterium sp NRC1	ATCC 33170
Thermus thermophilus	ATCC 27634
Deinococcus radiodurans	ATCC 13939
Saccharomyces cerevisiae	ATCC 10751
Schizosaccharomyces pombe	ATCC 24969
Xylella fastidiosa	ATCC 35881
Emericella nidulans	ATCC 36104
Mesorhizobium loti	ATCC 35173
Acremonium crysogenum	ATCC 11550
Pseudomonas putida	ATCC 47054

Staphylococcus aureus	ATCC 35556

5. A method as claimed in any of the preceding claims, wherein the metA-encoding sequence comprises a coding sequence according to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43 and 45 or a nucleotide sequence homologous thereto which codes for a protein with metA activity.

6. A method as claimed in any of the preceding claims, wherein the metA-encoding sequence codes for a protein with metA activity, said protein comprising an amino acid sequence according to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44 and 46 or an amino acid sequence homologous thereto which represents a protein with metA activity.

7. A method as claimed in any of the preceding claims, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. A method as claimed in claim 7, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or
b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

9. A method as claimed in any of the preceding claims, wherein the coding metA sequence is overexpressed.

10. A method as claimed in any of the preceding claims, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of the desired sulfur-containing fine chemical has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

11. A method as claimed in any of the preceding claims, wherein bacteria are fermented in which at least one metabolic pathway, which reduces the production of the desired sulfur-containing fine chemical, is at least partially switched off.

12. A method as claimed in any of the preceding claims, wherein coryneform bacteria are

fermented in which, at the same time, at least one of the genes selected from among

a) the gene lysC, which encodes an aspartate kinase,
b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene gap,
c) the 3-phosphoglycerate kinase-encoding gene pgk,
d) the pyruvate carboxylase-encoding gene pyc,
e) the triose phosphate isomerase-encoding gene tpi,
f) the methylene tetrahydrofolate reductase-encoding gene metF,
g) the cystathionine gamma-synthase-encoding gene metB,
h) the cystathionine gamma-lyase-encoding gene metC,
i) serine hydroxymethyltransferase-encoding gene glyA,
j) the O-acetylhomoserine sulfhydrylase-encoding gene metY,
k) the vitamin B12-dependent methionine synthase-encoding gene metH,
l) the phosphoserine aminotransferase-encoding gene serC,
m) the phosphoserine phosphatase-encoding gene serB,
n) the serine acetyltransferase-encoding gene cysE, and
o) the gene hom, which encodes a homoserine dehydrogenase,

is overexpressed or mutated in such a way that the activity of the corresponding proteins is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins.

13. A method as claimed in any of the preceding claims, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

a) the homoserine kinase-encoding gene thrB,
b) the threonine dehydratase-encoding gene ilvA,
c) the threonine synthase-encoding gene thrC,
d) the meso-diaminopimelate D-dehydrogenase-encoding gene ddh,
e) the phosphoenolpyruvate carboxykinase-encoding gene pck,
f) the glucose-6-phosphate 6-isomerase-encoding gene pgi,
g) the pyruvate oxidase-encoding gene poxB,
h) the dihydrodipicolinate synthase-encoding gene dapA,
i) the dihydrodipicolinate reductase-encoding gene dapB; and
j) the diaminopicolinate decarboxylase-encoding gene,

is attenuated by changing the rate of expression or by introducing a specific mutation.

14. A method as claimed in one or more of the preceding claims, wherein microorganisms of the species Corynebacterium glutamicum are used.

15. A method for producing an L-methionine-containing animal feed additive from fermentation broths, which comprises the following steps:

a) culturing and fermentation of an L-methionine-producing microorganism in a fermentation medium;

b) removal of water from the L-methionine-containing fermentation broth;

c) removal of from 0 to 100% by weight of the biomass formed during fermentation; and

d) drying of the fermentation broth obtained according to b) and/or c), in order to obtain the animal feed additive in the desired powder or granule form.

16. A method as claimed in claim 15, wherein microorganisms according to the definition in any of claims 1 to 14 are used.